

BIOGRAPHICAL SKETCH

NAME: Ounit, Rachid, Ph.D,

POSITION TITLE: Expert in Sequencing Technologies, Bioinformatics and Genomics

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Lycée d'État Henri Wallon, Valenciennes, France	B.Sc.	06/2006	Mathematics & Physics
E.N.S.I.I.E., Évry, France	M.Sc.	10/2010	Computer Science & Business
University of California, Riverside, CA	Ph.D.	03/2017	Computer Science, Bioinformatics

A. Personal Statement

I love collaborating with scientists, physicians and engineers to drive the rapid advancement of scientific discovery in life sciences, especially in the context of the human health. My exceptional contributions in this pursuit are outlined below, reflecting my unwavering enthusiasm and dedication. I look forward to collaborating with like-minded individuals who share this mission.

B. Positions and Honors

Positions and Employment

2007	<i>Software Developer (Confidential clearance), Atomic Energy Commission, Bruyères-le-Châtel, Essonne, France</i>
2007-2009	<i>Project Manager, Diese, Évry, Essonne, France</i>
2008-2009	<i>Vice-President, Diese, Évry, Essonne, France</i>
2010	<i>Research Assistant, Courant Institute of Mathematical Sciences, New York University, NY</i>
2011-2012	<i>Software Engineer, Schlumberger R&E, Houston, TX</i>
2013-2017	<i>Research Assistant, University of California, Riverside, CA</i>
2014-2015	<i>Teaching Assistant, University of California, Riverside, CA</i>
2015	<i>Lecturer, University of California, Riverside, CA</i>
2016	<i>Bioinformatician, Biotia Inc, New York, NY</i>
2017-2020	<i>Chief Technology Officer, Biotia Inc, New York, NY</i>
2018-2020	<i>Director of the Board, Biotia Inc, New York, NY</i>
2020-2022	<i>Engineering Accelerating Science Lead, Karius Inc, Redwood City, CA</i>
2023	<i>Software Engineering Lead, Alamar Biosciences, Fremont, CA</i>

Other Experience and Professional Membership

2014	<i>Member, Association for Computing Machinery</i>
2015	<i>Member, International Society for Computational Biology</i>
2015	<i>Member, Metagenomics & Metadesign of Subways & Urban Biomes</i>
2017	<i>Member, Metagenomics Research Group at ABRF</i>
2017	<i>Member, Extreme Microbiome Project</i>
2019	<i>Member, NASA GeneLab Analysis Working Group</i>
2019	<i>Member, New York Academy of Sciences</i>

Honors

2012	Dean's Distinguished Fellowship, University of California, Riverside, CA
2013	Omicron Delta Kappa, National Leadership Honor Society
2014	ACM-BCB, Student Travel Award
2019	ABRF Waters Corporation Poster Award, ABRF Annual Meeting, San Antonio, TX

C. Peer-reviewed publications (3100+ Citations)

1. Muñoz-Amatriaín M, Lonardi S, Luo M, Madishetty K, Svensson JT, Moscou MJ, Wanamaker S, Jiang T, Kleinhofs A, Muehlbauer GJ, Wise RP, Stein N, Ma Y, Rodriguez E, Kudrna D, Bhat P, Chao S, Condamine P, Heinen S, Resnik J, Wing R, Witt HN, Alpert M, Beccuti M, Bozdogan S, Cordero F, **Ounit R**, Wu Y, You F, Zheng J, et al. Sequencing of 15 622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. *The Plant Journal*. 2015 Oct;84(1):216-27.
2. **Ounit R**, Wanamaker S, Close TJ, Lonardi S. CLARK: fast and accurate classification of metagenomic and genomic sequences using discriminative k-mers. *BMC genomics*. 2015 Dec;16(1):236.
3. Harris EY*, **Ounit R***, Lonardi S. BRAT-nova: fast and accurate mapping of bisulfite-treated reads. *Bioinformatics*. 2016 Feb 23;32(17):2696-8.
*Authors contributed equally
4. **Ounit R**, Lonardi S. Higher classification sensitivity of short metagenomic reads with CLARK-S. *Bioinformatics*. 2016 Aug 18;32(24):3823-5.
5. Hahn L, Leimeister CA, **Ounit R**, Lonardi S, Morgenstern B. Rasbhari: Optimizing spaced seeds for database searching, read mapping and alignment-free sequence comparison. *PLoS computational biology*. 2016 Oct 19;12(10):e1005107.
6. **Ounit R**, Computing the Microbiome: Faster, More Accurate and More Efficient Methods for the Analysis of Metagenomes. UC Riverside. ProQuest ID: Ounit_ocr_0032D_12788. Merritt ID: ark:/13030/m5hx670h
7. Lonardi S, Zhu T, Muñoz-Amatriaín M, Liang Q, Wanamaker S, **Ounit R**, Alhakami H, Luo MC, Close TJ. Assembly of eleven pseudomolecules representing the cowpea genome sequence. *Plant and Animal Genome XXV*, January. 2017:13-8.
8. Beier S, Himmelbach A, Colmsee C, Zhang XQ, Barrero RA, Zhang Q, Li L, Bayer M, Bolser D, Taudien S, Groth M, Felder M, Hastie A, Simkova H, Stankova H, Vrana J, Chan S, Munoz-Amatrain M, **Ounit R**, Wanamaker S, Schmutzer T, Aliyeva-Schnorr L, Grasso S, Tanskanen J, Sampath D, Heavens D. Construction of a map-based reference genome sequence for barley, *Hordeum vulgare* L. *Scientific data*. 2017 Apr 27;4:170044.
9. Mascher M, Gundlach H, Himmelbach A, Beier S, Twardziok SO, Wicker T, Radchuk V, Dockter C, Hedley PE, Russell J, Bayer M, Ramsay L, Liu H, Haberer G, Zhang XQ, Zhang Q, Barrero R, Li L, Taudien S, Groth M, Felder M, Hastie A, Munoz-Amatrain M, **Ounit R**, Wanamaker S, Bolser D, Colmsee C, Schmutzer T, Aliyeva-Schnorr L, Grasso S, Tanskanen J, Chailyan A, Sampath D, Heavens D., Clissold L, Cao S, Chapman B, Dai F, Han Y, Lua H, Li X, Lin C, McCooke JK, et al. A chromosome conformation capture ordered sequence of the barley genome. *Nature*. 2017 Apr;544(7651):427.
10. O'Hara NB, Reed HJ, Afshinnekoo E, Harvin D, Caplan N, Rosen G, Frye B, Woloszynek S, **Ounit R**, Levy S, Butler E. Metagenomic characterization of ambulances across the USA. *Microbiome*. 2017 Dec;5(1):125.
11. McIntyre AB, **Ounit R**, Afshinnekoo E, Prill RJ, Hénaff E, Alexander N, Minot SS, Danko D, Fook J, Ahsanuddin S, Tighe S. Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. *Genome biology*. 2017 Dec;18(1):182.
12. Lonardi S, Muñoz-Amatriaín M, Liang Q, Shu S, Wanamaker SI, Lo S, Tanskanen J, Schulman AH, Zhu T, Luo MC, Alhakami H, **Ounit R**, Hasan AMd, et al. The genome of cowpea (*Vigna unguiculata* [L.] Walp.). *The Plant Journal*. 2019 Jun;98(5), pp.767-782.
13. **Ounit R**, Mason C, Lonardi S, O'Hara N. A Metagenomic Analysis of Environmental and Clinical Samples Using a Secure Hybrid Cloud Solution. *Journal of Biomolecular Techniques: JBT*. 2019 Dec;30(Suppl):S2.

14. Danko D, Malli Mohan GB, Sierra MA, Rucker M, Singh NK, Regberg AB, Bell MS, O'Hara NB, **Ounit R**, Mason CE, Venkateswaran K. Characterization of spacesuit associated microbial communities and their implications for NASA missions. *Frontiers in Microbiology*. 2021:1900.
15. The International MetaSUB Consortium. A global metagenomic map of urban microbiomes and antimicrobial resistance. *Cell*. 2021 May 26.
16. Park SY, Lindner MS, Brick K, Noll N, **Ounit R**, Noa LJ, Sabzwari R, Triple R, Sniffen JC, Roth P, Khan A. Detection of Mpox virus using microbial cell-free DNA: the potential of pathogen-agnostic sequencing for rapid identification of emerging pathogens. *The Journal of Infectious Diseases*. 2023 Oct 12:jjad452.

D. Presentations

Posters

1. Salsgiver E, Martin E, Callan K, O'Hara NB, **Ounit R**, Westblade LF, Mason CE, Simon MS, Saiman L, Furuya EY, Calfee DP. 1154. Comparison of Five Testing Modalities for the Assessment of Patient Environment Cleanliness. In *Open Forum Infectious Diseases* 2018 Nov (Vol. 5, No. suppl_1, pp. S347-S347). US: Oxford University Press.
2. **Ounit R**, Mason CE, Lonardi S, O'Hara NB, A metagenomic analysis of environmental and clinical samples using a secure hybrid cloud solution. *ABRF Annual Meeting*, San Antonio, TX. March 2019.
3. **Ounit R**, Mason CE, Lonardi S, O'Hara NB. A secure analysis of environmental and clinical samples using a hybrid cloud profiler. *RECOMB*, Washington, DC. May 2019.
4. **Ounit R**, Nagy-Szakal D, Ford J, Viangteeravat T, Panmontha W, Rangsrakitphoti P, Techasathit W, Mason CE, O'Hara NB. Highly accurate Nanopore metagenomics and antibiotic resistance for clinical urine diagnostics, *AGBT Precision Health*, San Diego, CA. September 2019.
5. **Ounit R**, Nagy-Szakal D, Ford J, Viangteeravat T, Panmontha W, Rangsrakitphoti P, Techasathit W, Mason CE, O'Hara NB. Comprehensive and fast NGS-based profiling of the antimicrobial resistance in clinical urine samples. *AGBT Precision Health*, San Diego, CA. September 2019.
6. King E, Patel D, Roland R, Kessler J, Saini A, Jindal N, Nagy-Szakal D, **Ounit R**, O'Hara NB. 463. Evaluation of Trimethoprim-Sulfamethoxazole Utilization for Skin and Soft-Tissue Infections During Emergency Department Visits at Two Community Teaching Hospitals. In *Open Forum Infectious Diseases* 2019 Oct 2 (Vol. 6).

Talks & Panels

1. "Higher classification accuracy of short metagenomic reads by discriminative spaced k-mers", *15th International Workshop of Algorithms in Bioinformatics*, Atlanta, GA. September, 2015
2. "Classification of metagenomic sequences: how to make it faster and more accurate". *Seminar Series*, Center for Data Science, New York University, New York, NY. September, 2015
3. "Challenges in Integrating New Technology Based on Sequencing and Intelligent Systems in Healthcare Environments: Case of Hospital-Acquired Infections". *4th Translational Microbiome Conference*. Boston, MA. April, 2018.
4. "Artificial Intelligence Summit", Panelist for *Entre*. Microsoft Times Square, New York, NY. June, 2019.

E. Grants

1. "Characterization of the microbial population and bacterial replication rates from metagenomic samples of healthcare settings: Secure, faster, more accurate and scalable computational methods"
Principal Investigator. National Science Foundation (NSF) via XSEDE (eXtreme Science and Engineering Discovery Environment). 02/2018 – 08/2019
2. "Characterization of the Profile and Dynamics of the Antimicrobial Resistance in an International Hospital"
Principal Investigator, NSF via XSEDE. 03/2019 – 03/2020

F. Patent

U.S. Patent Application No. PCT/US2016/058862, filed on October 26, 2016 (*Patent Pending*).

G. Peer-Reviews (50+ reviews)

Journals

Bioinformatics (2014, 2016, 2018, 2019, 2021), *BMC Bioinformatics* (2015, 2016), *BMC Genomics* (2022), *Computational Biology & Chemistry* (2018), *Evolutionary Bioinformatics* (2018), *Eurasip Journal on Bioinformatics and Systems Biology* (2018), *Frontiers in Bioinformatics* (2022), *Genomics, Genome Biology* (2020, 2021, 2024), *GigaScience* (2018, 2019), *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (2017), *Journal of Genetic Engineering and Biotechnology* (2020), *Microbiome* (2022), *PLoS One* (2022), *PLoS Computational Biology* (2017), *Proteomics & Bioinformatics* (2018).

Conferences

ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (2015, 2016, 2018), *Combinatorial Pattern Matching* (2015), *Intelligent System for Molecular Biology and the European Conference on Computational Biology* (2014, 2015), *International Conference in Research in Computational Molecular Biology (RECOMB)* (2014-2016, 2019), *RECOMB Comparative Genomics (RECOMB-CG)* (2014), *Workshop on Algorithms in Bioinformatics* (2014, 2016).

H. Teaching Experience

Teaching Assistant, "CS 165 – Computer Security" Fall 2013
Department of Computer Science & Engineering, Undergraduate Program, UC Riverside, CA
Instructor: Chinya V. Ravishankar

Teaching Assistant, "CS 10 – Introduction of Computer Science" Fall 2013
Department of Computer Science & Engineering, Undergraduate Program, UC Riverside, CA
Instructor: Adam Koehler

Teaching Assistant, "CS 218 – Design and Analysis of Algorithms" Fall 2014
Department of Computer Science & Engineering, Graduate Program, UC Riverside, CA
Instructor: Stefano Lonardi

Teaching Assistant, "CS 14 – Introduction to Data Structures and Algorithms" Summer 2015
Department of Computer Science & Engineering, Undergraduate Program, UC Riverside, CA
Instructor: Ryan Rusich

Lecturer, "CS 100 – Software Construction" Summer 2015
Department of Computer Science & Engineering, Undergraduate Program, UC Riverside, CA

I. Technical Skills

Sequence & Genomics analysis	BLAST tools, BWA, Bowtie tools, CutAdapt, FastQC, FASTX-toolkit, GATK, Kraken tools, Metaphlan tools, MUMmer, Plink, RDP, SAMtools, Scythe/Sickle, Trimmomatic.
Epigenetics analysis	Bismark, BRAT, BSMAP, BS-Seeker.
Genome ssembly	Canu, Flye, Spades/MetaSpades.
Database/Cloud	MySQL, PostGreSQL. AWS Athena/RDS.
Programming Language	C, C++, C#, Fortran, Java, Matlab, OpenMP, Python, R, Shell, SQL, VBA, XML.
Workflow Management Software	Nextflow.
Web Development	Django, React/Javascript, PHP, HTML, CSS
Programming Framework	IntelliJ, Eclipse, Netbeans, .NET, Vim, Visual Studio.
Containers	Docker, Singularity.
Project Management	Asana, Atlassian Confluence, JIRA, Figma, LucidChart.
Software testing, design/modeling	Unit, Component, Regression and System testing, Design Patterns, UML.
CI/CD framework	Flake8, Travis, Jenkins.
Version control	Bitbucket, Github, Jupyter Notebooks.